

Abstract

We explored the honey bee (*Apis mellifera*) virome through extensive metagenomic analysis across two major projects, focusing on virome stability and longitudinal changes. The first project, which included 39 samples from Czechia, aimed to understand virome stability within triplicates, revealing varying viral compositions of honey bee-infecting viruses and was published in 2022. The second project extended the analysis to 48 samples over three years, we explored recent tools in viral metagenomics bioinformatics which led to the discovery of novel DNA viruses: *Apis mellifera* filamentous-like virus (AmFLV) and *Apis mellifera* nudivirus (AmNV), along with nine new genomes from the *Parvoviridae* family, tentatively named Bee densovirus 1 to 9. The longitudinal study highlighted significant viral abundance variability that may be influenced by factors such as pesticide exposure. An analysis comparing viral detection by proteomics and metagenomics was also conducted. These findings contribute to the understanding of honey bee virome dynamics and underscore the need for continued research into viral interactions and their ecological implications.

Keywords: metagenomics, viruses, honey bee, vMAGs